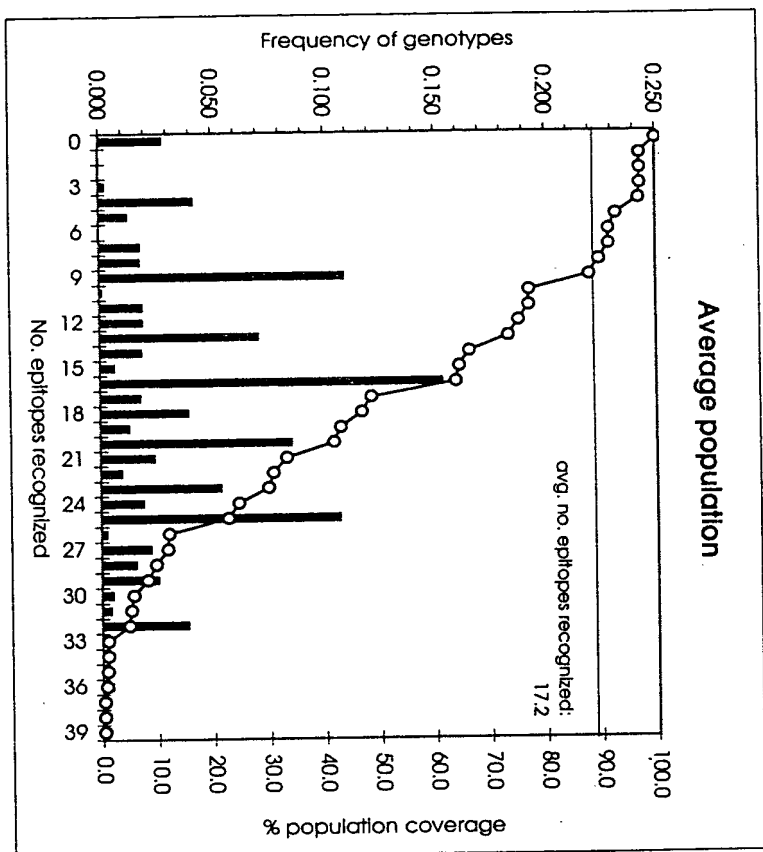


Figure 1



Plot of total frequency of genotypes as a function of the number of candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

09443333 100599

CMV	signal	pol 921	env 285	pol 961	nef 62	nef 94	gag 34	env 49	gag 397	env 293	env 134	pol 87	pol 70	pol 337	pol 91	vpr 72	pol 920	env 62	pol 476	pol 919
A3	B7	A3	A2	A3	A2	A3	A2	A3	A2	A3	A2	A2	A2	A3	A3	A3	A2	A3	B7	A3

